Search summaries for 10/767701

```
<!--StartFragment-->Database :          A_Geneseq_21:*
                   1:  geneseqp1980s:*
                   2:  geneseqp1990s:*
                   3:  geneseqp2000s:*
                   4:  geneseqp2001s:*
                   5:  geneseqp2002s:*
                   6:  geneseqp2003as:*
                   7:  geneseqp2003bs:*
                   8:  geneseqp2004s:*
                   9:  geneseqp2005s:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being pr:
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1131	100.0	244	8	ADY04217	Ady04217 P:
2	1131	100.0	244	8	ADX67363	Adx67363 P:
3	1131	100.0	244	8	ADX88676	Adx88676 P:
4	1125	99.5	220	3	AAG44786	Aag44786 Z(
5	1116	98.7	225	8	ADX94502	Adx94502 P:
6	1106	97.8	215	8	ADX73118	Adx73118 P:
7	1098	97.1	283	8	ADX73919	Adx73919 P:
8	1098	97.1	283	8	ADX89391	Adx89391 P:
9	1098	97.1	285	8	ADY13717	Ady13717 P:
10	1094	96.7	287	8	ADY07764	Ady07764 P:
11	1093	96.6	232	8	ADX78995	Adx78995 P:
12	1093	96.6	233	8	ADX67693	Adx67693 P:
13	1016	89.8	220	3	AAG31748	Aag31748 A:
14	1013	89.6	220	3	AAB32549	Aab32549 E(
15	1010	89.3	219	3	AAG17011	Aag17011 A:
16	1003	88.7	220	3	AAG40308	Aag40308 A:
17	995	88.0	221	3	AAG44461	Aag44461 A:
18	995	88.0	221	3	AAG47167	Aag47167 A:
19	995	88.0	222	3	AAB32874	Aab32874 P:
20	963	85.1	225	8	ADT59055	Adt59055 P:
21	944	83.5	184	3	AAG44787	Aag44787 Z(
22	873.5	77.2	236	8	ADX79239	Adx79239 P:
23	858	75.9	234	8	ADX66514	Adx66514 P:
24	819	72.4	221	8	ADX67826	Adx67826 P:
25	784	69.3	232	8	ADX67636	Adx67636 P:
26	744	65.8	155	3	AAB32593	Aab32593 E(
27	740	65.4	161	3	AAB32883	Aab32883 P:
28	732.5	64.8	240	3	AAG54006	Aag54006 A:
29	732.5	64.8	240	3	AAG54005	Aag54005 A:

30	732.5	64.8	240	3	AAG44288	Aag44288 A₁
31	732.5	64.8	240	3	AAG11705	Aag11705 A₁
32	732.5	64.8	274	8	ADX67307	Adx67307 P:
33	732.5	64.8	502	3	AAG53974	Aag53974 A₁
34	732.5	64.8	558	3	AAG53973	Aag53973 A₁
35	732.5	64.8	664	3	AAG53972	Aag53972 A₁
36	718	63.5	166	3	AAG30424	Aag30424 A₁
37	718	63.5	175	3	AAG30423	Aag30423 A₁
38	714	63.1	257	8	ADY06189	Ady06189 P:
39	712	63.0	247	8	ADY22656	Ady22656 P:
40	712	63.0	278	8	ADX88674	Adx88674 P:
41	711	62.9	155	3	AAG37515	Aag37515 A₁
42	699	61.8	139	3	AAG44785	Aag44785 Z₍
43	695	61.5	150	3	AAB32605	Aab32605 E₁
44	650	57.5	141	3	AAG17012	Aag17012 A₁
45	650	57.5	141	3	AAG30425	Aag30425 A₁

```
<!--StartFragment-->Database :        UniProt_05.80:*
                1:   uniprot_sprot:*
                2:   uniprot_trembl:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being pr:
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1100	97.3	220	2	Q69WS1_ORYSA	Q69ws1 ory:
2	1091	96.5	220	2	Q84SZ1_ORYSA	Q84sz1 ory:
3	1016	89.8	285	1	VA725_ARATH	O48850 aral
4	1010	89.3	219	1	VA721_ARATH	Q9ztw3 aral
5	1010	89.3	219	2	Q681L9_ARATH	Q681l9 aral
6	1006	88.9	219	2	Q681H0_ARATH	Q681h0 aral
7	1003	88.7	220	1	VA726_ARATH	Q9mas5 aral
8	995	88.0	221	1	VA722_ARATH	P47192 aral
9	933	82.5	194	2	Q7X9C5_PYRPY	Q7x9c5 pyr\
10	848.5	75.0	222	1	VA724_ARATH	O23429 aral
11	848.5	75.0	222	2	Q6ID96_ARATH	Q6id96 aral
12	795	70.3	215	2	Q5URW2_HORVD	Q5urw2 hor(
13	792	70.0	217	1	VA723_ARATH	Q8vy69 aral
14	786	69.5	218	2	Q6RUK8_TRIMO	Q6ruk8 tri(
15	779	68.9	181	2	Q67YV9_ARATH	Q67yv9 aral
16	741.5	65.6	248	2	Q8H3D2_ORYSA	Q8h3d2 ory:
17	732.5	64.8	240	1	VA727_ARATH	Q9m376 aral
18	732.5	64.8	240	2	Q53XE0_ARATH	Q53xe0 aral
19	715	63.2	241	2	Q6YZI8_ORYSA	Q6yzi8 ory:
20	413.5	36.6	219	1	VA711_ARATH	O49377 aral
21	407	36.0	221	1	VA713_ARATH	Q9lfp1 aral
22	396	35.0	221	1	VA714_ARATH	Q9fmr5 aral
23	394.5	34.9	260	2	Q86AQ7_DICDI	Q86aq7 dic(
24	387	34.2	220	2	Q6DDH7_XENLA	Q6ddh7 xen(
25	384	34.0	220	2	Q5ZL74_CHICK	Q5zl74 gal:
26	383	33.9	220	2	P70280_MOUSE	P70280 m s\
27	380	33.6	219	1	SYBL1_HUMAN	P51809 hom(
28	380	33.6	220	2	Q53GY7_HUMAN	Q53gy7 hom(
29	379	33.5	87	2	Q4U3F2_IPOBA	Q4u3f2 ipo(
30	377.5	33.4	219	1	VA712_ARATH	Q9siq9 aral
31	377	33.3	219	1	SYBL1_PONPY	Q5rf94 pon(
32	377	33.3	220	2	Q9JHW5_RAT	Q9jhw5 rat(
33	372	32.9	221	2	Q9LWK1_ORYSA	Q9lwk1 ory:
34	360	31.8	223	2	Q8S670_ORYSA	Q8s670 ory:
35	346.5	30.6	226	2	Q69SJ1_ORYSA	Q69sj1 ory:
36	343.5	30.4	218	2	Q9V5C3_DROME	Q9v5c3 dro:

37	338.5	29.9	228	2	Q7Z0P6_PARTE	Q7z0p6	par:
38	338.5	29.9	306	2	Q560P1_CRYNE	Q560p1	cry;
39	338.5	29.9	306	2	Q5KPN8_CRYNE	Q5kpn8	cry;
40	338	29.9	208	2	Q8IET3_PLAF7	Q8iet3	pla:
41	332	29.4	208	2	Q4YCD2_PLABE	Q4ycd2	pla:
42	327	28.9	216	2	Q54NW7_DICDI	Q54nw7	dic!
43	321	28.4	218	2	Q7QED7_ANOGA	Q7qed7	ano;
44	302.5	26.7	242	2	Q7S9T6_NEUCR	Q7s9t6	neu:
45	299	26.4	236	2	Q4I187_GIBZE	Q4i187	gib!

<!--EndFragment-->

```
<!--StartFragment-->Database :          PIR_80:*
                1:  pir1:*
                2:  pir2:*
                3:  pir3:*
                4:  pir4:*
```

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score greater than or equal to the score of the result being pr:
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1016	89.8	220	2	T00801	probable s>
2	995	88.0	221	2	F84741	probable s>
3	988.5	87.4	229	2	F86180	hypothetic:
4	732.5	64.8	240	2	T47589	synaptobre'
5	718	63.5	175	2	D86180	hypothetic:
6	646.5	57.2	212	2	E84741	probable s>
7	413.5	36.6	219	2	T04630	synaptobre'
8	411.5	36.4	159	2	B71423	hypothetic:
9	377.5	33.4	219	2	C84647	probable s>
10	377	33.3	220	2	JC7258	vesicle-as:
11	295	26.1	69	2	E86180	hypothetic:
12	274	24.2	60	2	D44088	homeotic p:
13	200.5	17.7	121	2	T39073	synaptobre'
14	185	16.4	117	2	S31250	synaptobre'
15	185	16.4	223	2	S47654	integral m(
16	175	15.5	109	2	T33239	synaptobre'
17	174.5	15.4	115	2	S62059	synaptobre'
18	174.5	15.4	719	2	E88504	protein B0:
19	169.5	15.0	132	2	JC1522	synaptobre'
20	169.5	15.0	152	2	JC1521	synaptobre'
21	167.5	14.8	116	2	B38315	synaptobre'
22	167.5	14.8	116	2	JN0011	synaptobre'
23	167.5	14.8	116	2	B34288	synaptobre'
24	160	14.1	211	2	T13477	synaptobre'
25	153	13.5	125	2	S40153	synaptobre'
26	149.5	13.2	118	2	S52747	Vamp1 prot(
27	149.5	13.2	118	2	A38315	synaptobre'
28	147	13.0	118	2	A34288	vesicle-as:
29	145.5	12.9	120	2	A32146	vesicle-as:
30	145.5	12.9	209	2	T40099	probable s>
31	145.5	12.9	251	2	S64927	probable m(
32	143.5	12.7	103	2	S35077	cellubrevi:
33	142	12.6	260	2	T09023	hypothetic:
34	138.5	12.2	508	2	F86458	unknown pr(

35	136.5	12.1	198	2	JE0228	Xsnare 1 pɪ
36	128	11.3	254	2	T04067	hypotheticɛ
37	128	11.3	263	2	C86253	hypotheticɛ
38	120	10.6	145	2	T21318	hypotheticɛ
39	118.5	10.5	197	2	T39412	hypotheticɛ
40	115.5	10.2	110	2	S35107	hypotheticɛ
41	114	10.1	200	2	T52162	probable sɪ
42	111	9.8	200	2	S38033	cell divis:
43	97	8.6	257	2	A89456	protein F5!
44	95	8.4	102	2	S44781	C30A5.4 prɾ
45	94.5	8.4	102	2	T24909	hypotheticɛ

<!--EndFragment-->